

**FIGURE 1**

Target segment starts with AA Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
AATGTCCACATGTCAGGAGGC [SEQ ID NO:11]	0.52	93	UGUCCACAUGUCAGGAGGCUU [SEQ ID NO:29] UUACAGGUGUACAGUCCUCCG [SEQ ID NO:47]
AACAAGACTGGACCATCCAGT [SEQ ID NO:12]	0.48	124	CAAGACUGGACCAUCCAGUUU [SEQ ID NO:30] UUGUUCUGACCUGGUAGGUCA [SEQ ID NO:48]
AAGTGCCTCCAGCACTATTGT [SEQ ID NO:13]	0.48	246	GUGCGUCCAGCACUAUUGUUU [SEQ ID NO:31] UUCACGCAGGUCGUGAUAAACA [SEQ ID NO:49]
AACCTCAAGATCCACAGCAGC [SEQ ID NO:14]	0.52	648	CCUCAAGAUCCACAGCAGCUU [SEQ ID NO:32] UUGGAGUUCUAGGUGUCGUCG [SEQ ID NO:50]
AAGTACTGGATGTCTCAGACG [SEQ ID NO:15]	0.48	888	GUACUGGAUGUCUCAGACGUU [SEQ ID NO:33] UUCAUGACCUACAGAGUCUGC [SEQ ID NO:51]
AAGGTTAGTCCGGACAGAGTC [SEQ ID NO:16]	0.52	1037	GGUUAGUCCGGACAGAGUCUU [SEQ ID NO:34] UUCCAAUCAGGCCUGUCUCAG [SEQ ID NO:52]
AAGCCACCTCGCTATTCAGAC [SEQ ID NO:17]	0.52	1089	GCCACCUCGCUAUUCAGACUU [SEQ ID NO:35] UUCGGUGGAGCGAUAAAGUCUG [SEQ ID NO:53]
AAGAACTTCAACCTGCCAGCA [SEQ ID NO:18]	0.48	1305	GAACUUCAACCUGCCAGCAUU [SEQ ID NO:36] UUCUUGAAGUUGGACGGUCGU [SEQ ID NO:54]
AACTTCAACCTGCCAGCATCC [SEQ ID NO:19]	0.52	1308	CUUCAACCUGCCAGCAUCCUU [SEQ ID NO:37] UUGAAGUUGGACGGUCGUAGG [SEQ ID NO:55]

AATTGAAGTGGAGCCAACGTC [SEQ ID NO:20]	0.48	1463	UUGAAGUGGAGCCAACGUCUU [SEQ ID NO:38] UUAACUUCACCUCGGUUGCAG [SEQ ID NO:56]
AACGTCGGAGAATGAAGAGGT [SEQ ID NO:21]	0.48	1478	CGUCGGAGAAUGAAGAGGUUU [SEQ ID NO:39] UUGCAGCCUCUACUUCUCCA [SEQ ID NO:57]
AAGAGTCAGAGGATGACTTCG [SEQ ID NO:22]	0.48	1513	GAGUCAGAGGAUGACUUCGUU [SEQ ID NO:40] UUCUCAGUCUCCUACUGAAGC [SEQ ID NO:58]
AACCAGGCAGATTGCTCAAGA [SEQ ID NO:23]	0.48	1922	CCAGGCAGAUUGCUCAGAUAU [SEQ ID NO:41] UUGGUCCGUCUAACGAGUUCU [SEQ ID NO:59]
AACGTCTTCTATGACAACGGC [SEQ ID NO:24]	0.48	2007	CGUCUUCUAUGACAACGGCUU [SEQ ID NO:42] UUGCAGAAGAUACUGUUGCCG [SEQ ID NO:60]
AACTGCGCATCCAGAATGGCT [SEQ ID NO:25]	0.52	2098	CUGCGCAUCCAGAAUGGCUUU [SEQ ID NO:43] UUGACGCGUAGGUCUUACCGA [SEQ ID NO:61]
AATCTGGTATGAACTCCACGC [SEQ ID NO:26]	0.48	2222	UCUGGUAUGAACUCCACGCUU [SEQ ID NO:44] UUAGACCAUACUUGAGGUGCG [SEQ ID NO:62]
AACCTCAGCCAGATTGGCATG [SEQ ID NO:27]	0.52	2313	CCUCAGCCAGAUUGGCAUGUU [SEQ ID NO:45] UUGGAGUCGGUCUAACCGUAC [SEQ ID NO:63]
AAGAGAGACCTACCTTCACCA [SEQ ID NO:28]	0.48	2383	GAGAGACCUACCUUCACCAUU [SEQ ID NO:46] UUCUCUCUGGAUGGAAGUGGU [SEQ ID NO:64]

**Target segment starts with CA**

Target segment: 5' -> 3'

	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
CAGGAATGTCCACATGTCAGG [SEQ ID NO:65]	0.52	89	GGAAUGUCCACAUGUCAGGUU [SEQ ID NO:94] UUCCUACAGGUGUACAGUCC [SEQ ID NO:123]

CACATGTCAGGAGGCAACCTT [SEQ ID NO:66]	0.52	99	CAUGUCAGGAGGCAACCUUUU [SEQ ID NO:95] UUGUACAGUCCUCCGUUGGAA [SEQ ID NO:124]
CAAGTGCGTCCAGCACTATTG [SEQ ID NO:67]	0.52	245	AGUGCGUCCAGCACUAUUGUU [SEQ ID NO:96] UUUCACGCAGGUCGUGAUAAAC [SEQ ID NO:125]
CAGCACTATTGTCACACCAGC [SEQ ID NO:68]	0.52	255	GCACUAUUGUCACACCAGCUU [SEQ ID NO:97] UUCGUGAUAAACAGUGUGGUCG [SEQ ID NO:126]
CACACTGAGGCCAACTTCTCT [SEQ ID NO:69]	0.52	783	CACUGAGGCCAACUUCUCUUU [SEQ ID NO:98] UUGUGACUCCGGUUGAAGAGA [SEQ ID NO:127]
CAGAGATCTCGGCAACTCCAT [SEQ ID NO:70]	0.52	848	GAGAUUCUGGCAACUCCAUIIU [SEQ ID NO:99] UUCUCUAGAGCCGUUGAGGUA [SEQ ID NO:128]
CAACTCCATCAAGCACAGGTT [SEQ ID NO:71]	0.48	860	ACUCCAUCAAGCACAGGUUUU [SEQ ID NO:100] UUUGAGGUAGUUCGUGUCCAA [SEQ ID NO:129]
CACCAAGTACTGGATGTCTCA [SEQ ID NO:72]	0.48	884	CCAAGUACUGGAUGUCUCAUU [SEQ ID NO:101] UUGGUUCAUGACCUACAGAGU [SEQ ID NO:130]
CAAGTACTGGATGTCTCAGAC [SEQ ID NO:73]	0.48	887	AGUACUGGAUGUCUCAGACUU [SEQ ID NO:102] UUUCAUGACCUACAGAGUCUG [SEQ ID NO:131]
CATCTTCTGATCATCCACCGA [SEQ ID NO:74]	0.48	1005	UCUUCUGAUCAUCCACCGAUU [SEQ ID NO:103] UUAGAAGACUAGUAGGUGGCU [SEQ ID NO:132]
CAAGGTTAGTCCGGACAGAGT [SEQ ID NO:75]	0.52	1036	AGGUUAGUCCGGACAGAGUUU [SEQ ID NO:104] UUUCCAAUCAGGCCUGUCUCA [SEQ ID NO:133]
CAGACCTGCACATCAGTCAGA [SEQ ID NO:76]	0.52	1105	GACCUGCACAUCAGUCAGAUU [SEQ ID NO:105] UUCUGGACGUGUAGUCAGUCU [SEQ ID NO:134]

CACACGGCAGCAGAAGAAGCTT [SEQ ID NO:77]	0.52	1292	CACGGCAGCAGAAGAACUUUU [SEQ ID NO:106] UUGUGCCGUCGUCUUCUUGAA [SEQ ID NO:135]
CACGGCAGCAGAAGAAGCTTCA [SEQ ID NO:78]	0.52	1294	CGGCAGCAGAAGAACUUCAUU [SEQ ID NO:107] UUGCCGUCGUCUUCUUGAAGU [SEQ ID NO:136]
CAGCAGAAGAAGCTTCAACCTG [SEQ ID NO:79]	0.48	1299	GCAGAAGAACUUCAACCGUU [SEQ ID NO:108] UUCGUCUUCUUGAAGUUGGAC [SEQ ID NO:137]
CAGAAGAAGCTTCAACCTGCCA [SEQ ID NO:80]	0.48	1302	GAAGAACUUCAACCGCCAUU [SEQ ID NO:109] UUCUUCUUGAAGUUGGACGGU [SEQ ID NO:138]
CAACGTCGGAGAATGAAGAGG [SEQ ID NO:81]	0.52	1477	ACGUCGGAGAAUGAAGAGGUU [SEQ ID NO:110] UUUGCAGCCUCUACUUCUCC [SEQ ID NO:139]
CATGATGAGGCCGAAGAGTCA [SEQ ID NO:82]	0.52	1500	UGAUGAGGCCGAAGAGUCAUU [SEQ ID NO:111] UUACUACUCCGGCUUCUCAGU [SEQ ID NO:140]
CAGAGGATGACTTCGAGGAGA [SEQ ID NO:83]	0.52	1519	GAGGAUGACUUCGAGGAGAUU [SEQ ID NO:112] UUCUCCUACUGAAGCUCCUCU [SEQ ID NO:141]
CAGACCAGCATCTTCCTTCAG [SEQ ID NO:84]	0.52	1587	GACCAGCAUCUCCUUCAGUU [SEQ ID NO:113] UUCUGGUCGUAGAAGGAAGUC [SEQ ID NO:142]
CAGCATCTTCCTTCAGGAGTG [SEQ ID NO:85]	0.52	1592	GCAUCUCCUUCAGGAGUGUU [SEQ ID NO:114] UUCGUAGAAGGAAGUCCUCAC [SEQ ID NO:143]
CATCCGGCTGATTGACATTGA [SEQ ID NO:86]	0.48	1706	UCCGGCUGAUUGACAUUGAUU [SEQ ID NO:115] UUAGGCCGACUAACUGUAACU [SEQ ID NO:144]
CATCATCACCAGCCTCTGTAA [SEQ ID NO:87]	0.48	1844	UCAUCACCAGCCUCUGUAAUU [SEQ ID NO:116] UUAGUAGUGGUCGGAGACAUU [SEQ ID NO:145]

CATCCAGAATGGCTGGCTATG [SEQ ID NO:88]	0.52	2105	UCCAGAAUGGCUGGCUAUGUU [SEQ ID NO:117] UUAGGUCUUACCGACCGAUAC [SEQ ID NO:146]
CAATCTGGTATGAACTCCACG [SEQ ID NO:89]	0.48	2221	AUCUGGUAUGAACUCCACGUU [SEQ ID NO:118] UUUAGACCAUACUUGAGGUGC [SEQ ID NO:147]
CAACCAGCAGAGGCAATAATC [SEQ ID NO:90]	0.48	2265	ACCAGCAGAGGCAAUAUUCUU [SEQ ID NO:119] UUUGGUCGUCUCCGUUAUUAG [SEQ ID NO:148]
CAGCAGAGGCAATAATCTGGC [SEQ ID NO:91]	0.52	2269	GCAGAGGCAAUAUUCUGGCUU [SEQ ID NO:120] UUCGUCUCCGUUAUUAGACCG [SEQ ID NO:149]
CAACCTCAGCCAGATTGGCAT [SEQ ID NO:92]	0.52	2312	ACCUCAGCCAGAUUGGCAUUU [SEQ ID NO:121] UUUGGAGUCGGUCUAACCGUA [SEQ ID NO:150]
CAAGAAGAGAGACCTACCTTC [SEQ ID NO:93]	0.48	2379	AGAAGAGAGACCUACCUUCUU [SEQ ID NO:122] UUUCUUCUCUCUGGAUGGAAG [SEQ ID NO:151]

**Target segment starts with GA**

Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
GAATGTCCACATGTCAGGAGG [SEQ ID NO:152]	0.52	92	AUGUCCACAUGUCAGGAGGUU [SEQ ID NO:181] UUUACAGGUGUACAGUCCUCC [SEQ ID NO:210]
GAAGAAGAACAAGCTGAAGCC [SEQ ID NO:153]	0.48	476	AGAAGAACAAGCUGAAGCCUU [SEQ ID NO:182] UUUCUUCUUGUUCGACUUCGG [SEQ ID NO:211]
GAACCTCAAGATCCACAGCAG [SEQ ID NO:154]	0.52	647	ACCUCAAGAUCACAGCAGUU [SEQ ID NO:183] UUUGGAGUUCUAGGUGUCGUC [SEQ ID NO:212]
GAGATCTCGGCAACTCCATCA [SEQ ID NO:155]	0.52	850	GAUCUCGGCAACUCCAUCAUU [SEQ ID NO:184] UUCUAGAGCCGUUGAGGUAGU [SEQ ID NO:213]

GATCTCGGCAACTCCATCAAG [SEQ ID NO:156]	0.52	852	UCUCGGCAACUCCAUCAAGUU [SEQ ID NO:185] UUAGAGCCGUUGAGGUAGUUC [SEQ ID NO:214]
GATGTCTCAGACGTGCACAGT [SEQ ID NO:157]	0.52	896	UGUCUCAGACGUGCACAGUUU [SEQ ID NO:186] UUACAGAGUCUGCACGUGUCA [SEQ ID NO:215]
GAGGAGATCCAGCAAGGTTAG [SEQ ID NO:158]	0.52	1024	GGAGAUC CAGCAAGGUUAGUU [SEQ ID NO:187] UUC CUCUAGGUCGUUCCAAUC [SEQ ID NO:216]
GAGATCCAGCAAGGTTAGTCC [SEQ ID NO:159]	0.52	1027	GAUCCAGCAAGGUUAGUCCUU [SEQ ID NO:188] UUCUAGGUCGUUCCAAUCAGG [SEQ ID NO:217]
GAAGCCACCTCGCTATTCAGA [SEQ ID NO:160]	0.52	1088	AGCCACCUCGCUAUUCAGAUU [SEQ ID NO:189] UUUCGGUGGAGCGAUAAGUCU [SEQ ID NO:218]
GAAGAACTTCAACCTGCCAGC [SEQ ID NO:161]	0.52	1304	AGAAUUAACCUGCCAGCUU [SEQ ID NO:190] UUUCUUGAAGUUGGACGGUCG [SEQ ID NO:219]
GAAGTTCAACCTGCCAGCATC [SEQ ID NO:162]	0.52	1307	ACUUAACCUGCCAGCAUCUU [SEQ ID NO:191] UUUGAAGUUGGACGGUCGUAG [SEQ ID NO:220]
GACCTCGAATCCAATCTTGGA [SEQ ID NO:163]	0.48	1424	CCUCGAAUCCAAUCUUGGAUU [SEQ ID NO:192] UUGGAGCUUAGGUUAGAACCU [SEQ ID NO:221]
GAGCCAACGTCGGAGAATGAA [SEQ ID NO:164]	0.52	1473	GCCAACGUCGGAGAAUGAAUU [SEQ ID NO:193] UUCGGUUGCAGCCUCUACUU [SEQ ID NO:222]
GAAGAGTCAGAGGATGACTTC [SEQ ID NO:165]	0.48	1512	AGAGUCAGAGGAUGACUUCUU [SEQ ID NO:194] UUUCUCAGUCUCCUACUGAAG [SEQ ID NO:223]
GAGTCAGAGGATGACTTCGAG [SEQ ID NO:166]	0.52	1515	GUCAGAGGAUGACUUCGAGUU [SEQ ID NO:195] UUCAGUCUCCUACUGAAGCUC [SEQ ID NO:224]

GAGGATGACTTCGAGGAGATG [SEQ ID NO:167]	0.52	1521	GGAUGACUUCGAGGAGAUGUU [SEQ ID NO:196] UCCUACUGAAGCUCCUCUAC [SEQ ID NO:225]
GATGACTTCGAGGAGATGAAC [SEQ ID NO:168]	0.48	1524	UGACUUCGAGGAGAUGAACUU [SEQ ID NO:197] UUACUGAAGCUCCUCUACUUG [SEQ ID NO:226]
GACTTCGAGGAGATGAACCTG [SEQ ID NO:169]	0.52	1527	CUUCGAGGAGAUGAACCUGUU [SEQ ID NO:198] UUGAAGCUCCUCUACUUGGAC [SEQ ID NO:227]
GACCAGCATCTTCCTTCAGGA [SEQ ID NO:170]	0.52	1589	CCAGCAUCUCCUUCAGGAUU [SEQ ID NO:199] UUGGUCGUAGAAGGAAGUCCU [SEQ ID NO:228]
GACGCTCTATTCCGTTGTGAG [SEQ ID NO:171]	0.52	1871	CGCUCUAUCCGUUGUGAGUU [SEQ ID NO:200] UUGCGAGAUAAAGGCAACACUC [SEQ ID NO:229]
GAATCCTACACAAGGACCTCA [SEQ ID NO:172]	0.48	1978	AUCCUACACAAGGACCUCAUU [SEQ ID NO:201] UUUAGGAUGUGUCCUGGAGU [SEQ ID NO:230]
GAACGTCTTCTATGACAACGG [SEQ ID NO:173]	0.48	2006	ACGUCUUCUAUGACAACGGUU [SEQ ID NO:202] UUUGCAGAAGAUACUGUUGCC [SEQ ID NO:231]
GACACAGAGGAGGATAAGCTC [SEQ ID NO:174]	0.52	2163	CACAGAGGAGGAUAAGCUCUU [SEQ ID NO:203] UUGUGUCUCCUCCUAUUCGAG [SEQ ID NO:232]
GACATTCTTCTCTTGCTGG [SEQ ID NO:175]	0.48	2349	CAUUCUUCUCUUCUGCUGGUU [SEQ ID NO:204] UUGUAAGAAGAGAAGACGACC [SEQ ID NO:233]
GAACAAGAAGAGAGACCTACC [SEQ ID NO:176]	0.48	2376	ACAAGAAGAGAGACCUACCUU [SEQ ID NO:205] UUUGUUCUUCUCUCUGGAUGG [SEQ ID NO:234]
GAAGAGAGACCTACCTTCACC [SEQ ID NO:177]	0.52	2382	AGAGAGACCUACCUUCACCUU [SEQ ID NO:206] UUUCUCUCUGGAUGGAAGUGG [SEQ ID NO:235]

GAGAGACCTACCTTCACCAAG [SEQ ID NO:178]	0.52	2385	GAGACCUACCUUCACCAAGUU [SEQ ID NO:207] UUCUCUGGAUGGAAGUGGUUC [SEQ ID NO:236]
GAGACCTACCTTCACCAAGCT [SEQ ID NO:179]	0.52	2387	GACCUACCUUCACCAAGCUUU [SEQ ID NO:208] UUCUGGAUGGAAGUGGUUCGA [SEQ ID NO:237]
GACCTACCTTCACCAAGCTCA [SEQ ID NO:180]	0.52	2389	CCUACCUUCACCAAGCUCAUU [SEQ ID NO:209] UUGGAUGGAAGUGGUUCGAGU [SEQ ID NO:238]

**Target segment starts with TA**

Target segment: 5' -> 3'	GC Ratio	Position	siRNA Sense strand: 5' -> 3' siRNA Antisense strand: 3' -> 5'
TACTGGATGTCTCAGACGTGC [SEQ ID NO:239]	0.52	891	CUGGAUGUCUCAGACGUGCUU [SEQ ID NO:242] UUGACCUACAGAGUCUGCACG [SEQ ID NO:245]
TACGGAAGCCACCTCGCTATT [SEQ ID NO:240]	0.52	1084	CGGAAGCCACCUCGCUAUUUU [SEQ ID NO:243] UUGCCUUCGGUGGAGCGAUAA [SEQ ID NO:246]
TACCTTCACCAAGCTCATGGA [SEQ ID NO:241]	0.48	2393	CCUUCACCAAGCUCAUGGAUU [SEQ ID NO:244] UUGGAAGUGGUUCGAGUACCU [SEQ ID NO:247]



## FIGURE 2

### CLUSTAL W multiple sequence alignment results

MSF: 1005 Type: P Check: 5073

Name: hksr-1\_full\_cae84534\_1.pep oo Len: 1005 Check: 4093 Weight: 12.1  
 Name: mksr-1\_np\_038599.pep oo Len: 1005 Check: 1555 Weight: 12.7  
 Name: hksr-1\_partial\_aac50354\_1.pep oo Len: 1005 Check: 10 Weight: 10.7  
 Name: hksr-2\_aaq24226\_1.pep oo Len: 1005 Check: 732 Weight: 13.8  
 Name: mksr-2.pep oo Len: 1005 Check: 2473 Weight: 13.6  
 Name: dmksr\_np\_524236.pep oo Len: 1005 Check: 4070 Weight: 36.8  
 Name: ceksr\_aaa92436\_1.pep oo Len: 1005 Check: 2140 Weight: 26.8

	CA1				
	1				50
hKSR-1(full)	MDRAALRAAA	MGEKKEGGGG	GDAAAEEGGA	GAAASRALQQ	CGQLQKLIDI
mKSR-1	MDRAALRAAA	MGEKKEGGGG	G..AAADGGA	GAASRALQQ	CGQLQKLIDI
hKSR-1(partial)	.....	.....	.....	.....	.....
hKSR-2	.....	.....	.....	.....	.....
mKSR-2	.....	.....	.....	.....	.....
DmKSR	.....MS	SNNAPASAP	DTGSTNANDP	ISGSLSVDSN	LVIIQDMIDL
CeKSR	.....	.....	.....	.....	.....

  

	CA1				
	51				100
hKSR-1(full)	SIGSLRGLRT	KCAVSNDLTQ	QEIRTLEAKL	VRYICKQRQC	KLSVAPGERT
mKSR-1	SIGSLRGLRT	KCSVSNDLTQ	QEIRTLEAKL	VKYICKQQQS	KLSVTPSDRT
hKSR-1(partial)	.....	.....	.....	.....	.....
hKSR-2	.....MT	DEQVCETVEK	YGANREECAR	LNASLSCLRN	VHMSGGNLSK
mKSR-2	.....MT	DEQVCETVEK	YGANQEECAR	LNASLSCLRN	VHMSGGNLSK
DmKSR	SANHLEGLRT	QCAISSTLTQ	QEIRCLESKL	VRYFSELLLA	KMRLNERIPA
CeKSR	.....	.....	.....	.....	.....

  

	CA1				
	101				150
hKSR-1(full)	PELNSYPRFS	DWLYTFNVRP	EVV....QEI	PRDLTLDALL	EMNEAKVKET
mKSR-1	AELNSYPRFS	DWLYIFNVRP	EVV....QEI	PQELTLDALL	EMDEAKAKEM
hKSR-1(partial)	.....	.....	.....	.....	.....
hKSR-2	QDWTIQWPTT	ETGKENNPVC	PPE....PTP	WIRTHLSQSP	RVPSKCVQHY
mKSR-2	QDWIIQWPTT	EPGQESNPVC	PPE....PSP	WIRTHLSQSP	RVQTKCPQHF
DmKSR	NGLVPHTTGN	ELRQWLRVVG	LSQGTLTACL	ARLTTLQSL	RLSDEEIRQL
CeKSR	.....	.....	.....	.....	.....

  

	CA1				
	151				200
hKSR-1(full)	LRRCGASGDE	.....CGRL	QYALTCLRKV	TGLGGEHKED	SSWSSLDARR
mKSR-1	LRRWGASTEE	.....CSRL	QQALTCLRKV	TGLGGEHKMD	SGWSSTDARD
hKSR-1(partial)	.....	.....	.....	.....	.....
hKSR-2	CHTSPTPGAP	.....VYTH	VDRLTVDAYP	GLCPPPP.LE	SGHRSLPPSP
mKSR-2	CPTSPTPGTP	.....VYTQ	VDRLTVDAYP	NLCPPPPPLE	SGHRSLPPSP
DmKSR	LADSPSQREE	EELRRLTRAM	QNLKRCMESL	ESGTAASNND	PEQWHWDSWD
CeKSR	.....	.....MM	QTQVASRAGY	SNLPQFGAGI	AQDIKTQAIN

					CA2	
	201					230
hKSR-1 (full)	ESGSGPSTDT	LSAASLPWPP	GSSQLGRAGN	SAQGPRISIV	SALPASDSPT	
mKSR-1	SSLG.....	.....PPMD	MLSSLGRAGA	STQGPRISIV	SALPASDSPV	
hKSR-1 (partial)	.....	.....	.....	.....	.....	
hKSR-2	RQRHAVRTPP	RTPNIVTTVT	PPGTTPMRKK	NKLKPPGTPP	PSSRKLIHLI	
mKSR-2	RQRHVVRTPP	RTPNIVTTVT	PPGTTPMRKK	NKLKPPGTPP	PSSRKLIHLI	
DmKSR	RPTHIHRGSV	GNIGLGNNST	ASPRTHHRQH	GVKGKNSALA	NSTNFKSGRQ	
CeKSR	NLKECLKLTT	INRFLTSSYE	EDAKSVERKI	FSAVYQMTKI	GLIDREKREI	

	251					300
hKSR-1 (full)	PSFSEGLSDT	CIPLHASGRL	TPRALHSFIT	PPTTPQLRRH	TKLKPPRTTP	
mKSR-1	PSFSEGLSDS	CIPLHTSGRL	TPRALHSFIT	PPTTPQLRRH	AKLKPPRTTP	
hKSR-1 (partial)	..EFRHTSAL	TQHTAHTQHT	SAHTQHSFIT	PPTTPQLRRH	TKLKPPRTTP	
hKSR-2	PGFTALHRSK	SHEFQLGHRV	DEAHTPKAKK	KSKPLNLKIH	SSVGSCENIP	
mKSR-2	PGFTALHRSK	SHEFQLGNRV	DEANTPKAKK	KSKPLNLKIH	SGVGSCENIP	
DmKSR	SPSATEELNS	TQGSQTLTL	TPSPPNSPFT	PSSGLSSSLN	GTPQRSRGTP	
CeKSR	NAIWFTFVGL	SAQNIRHLEI	CSITDFNALF	SITNQELRSL	ADRGRLDVET	

	301					350
hKSR-1 (full)	PPSRK.....	.....	.....VFQ	LLPSFPTLTR	SKSHESQLGN	
mKSR-1	PPSRK.....	.....	.....VFQ	LLPSFPTLTR	SKSHESQLGN	
hKSR-1 (partial)	PPSRK.....	.....	.....VFQ	LLPSFPTLTR	SKSHESQLGN	
hKSR-2	SQQRSP... ..	.....LSER	SLRSFFVGH	PFLPSTPPVH		
mKSR-2	AQQRSP... ..	.....LSER	SLRSFFVGH	PFLPSTPPVH		
DmKSR	PPARKHQTL	SQSHVQVDGE	QLARNRLPTD	PSPDSHSSTS	SDIFVDPNTN	
CeKSR	KRKLLQS... ..	.....TVILQN	HWNAYHSRTS	SGSTDEPSGQ		

					CA3	
	351					400
hKSR-1 (full)	RIDDVSSMRF	DLSHGSPQMV	RRDIGLSVTH	RFSTKSWLSQ	VCHVCQKSMI	
mKSR-1	RIDDVTPMKF	ELPHGSPQLV	RRDIGLSVTH	RFSTKSWLSQ	VCNVCQKSMI	
hKSR-1 (partial)	RIDDVSSMRF	DLSHGSPQMV	RRDIGLSVTH	RFSTKSWLSQ	VCHVCQKSMI	
hKSR-2	TEANFSANTL	SVPRWSPQIP	RRDLGNSIKH	RFSTKYWMSQ	TCTVCCKGML	
mKSR-2	TEANFSANTL	SVPRWSPQIP	RRDLGNSIKH	RFSTKYWMSQ	TCTVCCKGML	
DmKSR	ASSGGSSSNV	LMVPCSPGVG	HVGMGHAIKH	RFTKALGFMA	TCTLCQKQVF	
CeKSR	STPAIVTPSP	KFNVPSSLVT	SAKMIQSSSM	GFATTPKSPK	TSSRLVHAIP	

					CA3	
	401					450
hKSR-1 (full)	FG.VKCKHCR	LKCHNKCTKE	APACRISFLP	...LTRLRR.	.....	
mKSR-1	FG.VKCKHCR	LKCHNKCTKE	APACRITFLP	...LARLRR.	.....	
hKSR-1 (partial)	FG.VKCKHCR	LKCHNKCTKE	APACRISFLP	...LTRLRR.	.....	
hKSR-2	FG.LKCKNCK	LKCHNKCTKE	APPCHLLIIH	RGDPARLVR.	.....	
mKSR-2	FG.LKCKNCK	LKCHNKCTKE	APPCHLLIIH	RGDPARLVR.	.....	
DmKSR	HRWMKCTDCK	YICKKSCAPH	VPPSCGLPRE	YVDEFRIKE	QGGYASLPHV	
CeKSR	HKWHRSTKFR	FSGDAVCHFC	QRPLGFGFLN	AWEKCRSCKW	KVHTQCKGRV	

					CA4	
	451					500
hKSR-1 (full)	...TESVPSD	INNPVDRAAE	PHFGTLPKAL	TKK.....EH	PPAMNHLDS	
mKSR-1	...TESVPSD	INNPVDRAAE	PHFGTLPKAL	TKK.....EH	PPAMN.LDSS	
hKSR-1 (partial)	...TESVPSD	INNPVDRAAE	PHFGTLPKAL	TKK.....EH	PPAMNHLDS	
hKSR-2	...TESVPCD	INNPLRKPPR	YSDLHISQTL	PKTNKINKDH	IPVPYQPDSS	
mKSR-2	...TESVPCD	INNPLRKPPR	YSDLHISQTL	PKTNKINKDH	IPVPYQPDSS	
DmKSR	HGAAGSPLV	KKSTLGKPLH	QQHGDSSSPS	SSCTSSSTPSS	PALFQQRERE	
CeKSR	GDSCGLTPDH	LRFLFDKLIQ	ENNGGMWKDP	QSVPGSRSMN	EPAFQFPDTA	

## CA4

	501				550
hKSR-1 (full)	SNPSSTTSST	PSSPAPFPTS	SNPSSATTP.	.....	.....
mKSR-1	SNPSSTTSST	PSSPAPFLT	SNPSSATTP.	.....	.....
hKSR-1 (partial)	SNPSSTTSST	PSSPAPFPTS	SNPSSATTP.	.....	.....
hKSR-2	SNPSSTTSST	PSSPAPPLPP	SATPPSPLH.	.....	.....
mKSR-2	SNPSSTTSST	PSSPAPPLPP	SATPPSPLH.	.....	.....
DmKSR	LDQAGSSSSA	NLLPTPSLGK	HQPSQFNFPN	VTVTSSGGSG	GVSLISNEPV
CeKSR	IDSSSSTNSS	APSTPALPAG	ISGNVSSLTA	PYR.....	.....SERK

## CA4

	551				600
hKSR-1 (full)	....PNPSPG	QRDSRFNFPA	AYFIHHRQQF	IFPDISAFAH	AAPLPEAADG
mKSR-1	....PNPSPG	QRDS.....	.....RF	SFPDISACSQ	AAPLSSTADS
hKSR-1 (partial)	....PNPSPG	QRDSRFNFPA	AYFIHHRQQF	IFPDISAFAH	AAPLPEAADG
hKSR-2	....PSPQCT	RQKKNFNLP	SHYYKYKQQF	IFPDVVPVPE	TPTRAPQVIL
mKSR-2	....PSPQCP	RQKKNFNLP	SHYYKYKQQF	IFPDVVPVPE	TPTRAPQVIL
DmKSR	PEQFPTAPAT	ANGGLDSLVS	SSNGHMSSLI	GSQTSNASTA	ATLTGSLVNS
CeKSR	FLFPDTENYS	VHNRLPILVI	SEGDHPTTTE	IQQETENHNK	SAAASMSGNI

	601				650
hKSR-1 (full)	TRLDDQPKAD	VLEAHEAEAE	EPEAGKSEAE	DDE.DEVDDL	PSSRRPWRG.
mKSR-1	TRLDDQPKTD	VLGVHEAEAE	EPEAGKSEAE	DDEDEVDDL	PSSRRPWRG.
hKSR-1 (partial)	TRLDDQPKAD	VLEAHEAEAE	EPEAGKSEAE	DDE.DEVDDL	PSSRRPWRG.
hKSR-2	HPVTSNPIL	GNPLLQIEVE	PTSENEEVHD	EAESEDDFE	EMNLSLLSAR
mKSR-2	HPVTSNTILE	GNPLLQIEVE	PTSENEESHN	EAESEDEFE	EMNLSLLSAR
DmKSR	TTTTSTCSFF	PRKLSTAGVD	KRTPFTSECT	DTHKSNDSDK	TVSLSGSAST
CeKSR	ESEGTIVANH	EDSTGSQEV	SEAAPSQEA	DKFNKRADGG	FTWERHAWNM

	651			CA5	700
hKSR-1 (full)	PISRKAS...	.....	.QTSVYLQEW	DIPFEQVELG	EPIGQGRWGR
mKSR-1	PISRKAS...	.....	.QTSVYLQEW	DIPFEQVELG	EPIGQGRWGR
hKSR-1 (partial)	PISRKAS...	.....	.QTSVYLQEW	DIPFEQVELG	EPIGQGRWGR
hKSR-2	SFPRKAS...	.....	.QTSIFLQEW	DIPFEQLEIG	ELIGKGRFGQ
mKSR-2	SFPRKAS...	.....	.QTSIFLQEW	DIPFEQLEIG	ELIGKGRFGQ
DmKSR	DSDRTPVRVD	STEDGDSGQW	RQNSISLKEW	DIPYGDLLLL	ERIGQGRFGT
CeKSR	STIRGPN...	.....A	QASWNEVTIQ	FETIEFDKQA	PIIGRGRFGK

## CA5

	701				750
hKSR-1 (full)	VHRGRWHGEV	AIRLLEMD.G	HNQDH.LKLF	KKEVMNYRQT	RHENVVLFMG
mKSR-1	VHRGRWHGEV	AIRLLEMD.G	HNQDH.LKLF	KKEVMNYRQT	RHENVVLFMG
hKSR-1 (partial)	VHRGRWHGEV	AIRLLEMD.G	HNQDH.LKLF	KKEVMNYRQT	RHENVVLFMG
hKSR-2	VYHGRWHGEV	AIRLIDIE.R	DNEDQ.LKAF	KREVMAYRQT	RHENVVLFMG
mKSR-2	VYHGRWHGEV	AIRLIDIE.R	DNEDQ.LKAF	KREVMAYRQT	RHENVVLFMG
DmKSR	VHRALWHGDV	AVKLLNEDYL	QDEHM.LETF	RSEVANFKNT	RHENLVLFMG
CeKSR	VLRGFHYGDV	AVKVYTMELI	SDASKKAEFF	KLEVSAYKNT	RHDNIALFLG

## CA5

	751				800
hKSR-1 (full)	ACMNPPHLAI	ITSFCKG.RT	LHSFVRDPKT	SLDINKTRQI	AQEIIKGMGY
mKSR-1	ACMNPPHLAI	ITSFCKG.RT	LHSFVRDPKT	SLDINKTRQI	AQEIIKGMGY
hKSR-1 (partial)	ACMNPPHLAI	ITSFCKG.RT	LHSFVRDPKT	SLDINKTRQI	AQEIIKGMGY
hKSR-2	ACMSPPHLAI	ITSLCKG.RT	LYSVVRDAKI	VLDVKNTRQI	AQEIVKGMGY
mKSR-2	ACMSPPHLAI	ITSLCKG.RT	LYSVVRDAKI	VLDVKNTRQI	AQEIVKGMGY
DmKSR	ACMNPPYLAI	VTSLCKG.NT	LYTYIHQRRE	KFAMNRTLLI	AQQIAQGMGY
CeKSR	YFMSDGQYGM	VMSLSKGSQS	LYTLLHVRE	KLDLATRKI	AQQICQAVSY

CA5					
	801				850
hKSR-1 (full)	LHAKGIVHKD	LKSKNVFYDN	GKVVITDFGL	FGISGVVREG	RRENQLKLSH
mKSR-1	LHAKGIVHKD	LKSKNVFYDN	GKVVITDFGL	FGISGVVREE	RRENQLKLSH
hKSR-1 (partial)	LHAKGIVHKD	LKSKNVFYDN	GKVVITDFGL	FGISGVVREG	RRENQLKLSH
hKSR-2	LHAKGILHKD	LKSKNVFYDN	GKVVITDFGL	FSISGVLQAG	RREDKLRION
mKSR-2	LHAKGILHKD	LKSKNVFYDN	GKVVITDFGL	FSISGVLQAG	RRDDKLRION
DmKSR	LHAREIIHKD	LRTKNIFIEN	GKVIITDFGL	FSSTKLLYCD	MG...LGVPH
CeKSR	LHTKKILHKD	LRSKNILLES	KNKVITDFG	ILSMKRLAHP	KQKSGYLTSK

CA5					
	851				900
hKSR-1 (full)	DWLCYLAPEI	VREMPGKDE	...DQLPFSK	AADVYAFGTV	WYELQARDWP
mKSR-1	DWLCYLAPEI	VREMIPGRDE	...DQLPFSK	AADVYAFGTV	WYELQARDWP
hKSR-1 (partial)	DWLCYLAPEI	VREMPGKDE	...DQLPFSK	AADVYAFGTV	WYELQARDWP
hKSR-2	GWLCHLAPEI	IRQLSPDTEE	...DKLPFSK	HSDVFALGTI	WYELHAREWP
mKSR-2	GWLCHLAPEI	IRQLSPDTEE	...DKLPFSK	HSDVFALGTI	WYELHAREWP
DmKSR	NWLCYLAPEL	IRALQPEKPR	G..ECLEFTP	YSDVVSFGTV	WYELICGEFT
CeKSR	FWTNYIAPEL	AMAMRTEYDE	YECDDFPFSE	NSDVYAFGCV	WFEMLTGALP

CA5					
	901				950
hKSR-1 (full)	LKNQAAEASI	WQIGSGEGMK	RVLTSVSLGK	EVSEILSACW	AFDLQERPSF
mKSR-1	FKHQPAEALI	WQIGSGEGVR	RVLASVSLGK	EVGEILSACW	AFDLQERPSF
hKSR-1 (partial)	LKNQAAEASI	WQIGSGEGMK	RVLTSVSLGK	EVSEILSACW	AFDLQERPSF
hKSR-2	FKTQPAEAI	WQMG TG..MK	PNLSQIGMGK	EISDILLFCW	AFEQEERPTF
mKSR-2	FKTQPAEAI	WQMG TG..MK	PNLSQIGMGK	EISDILLFCW	AFEQEERPTF
DmKSR	FKDQPAESII	WQVGRG..MK	QSLANLQSGR	DVKDLLMLCW	TYEKEHRPQF
CeKSR	YAGELPHQIL	FAKTQG..IR	PVLPNVKCTQ	ELKELLVSCW	NTAPQDRPTL

CA5					
	951				1000
hKSR-1 (full)	SLLMDMLEKL	PK..LNRRLS	HPGHFWKSAD	INSSKVVPFR	ERFGLGVLES
mKSR-1	SLLMDMLERL	PK..LNRRLS	HPGHFWKSAD	INSSKVMPFR	ERFGLGTLES
hKSR-1 (partial)	SLLMDMLEKL	PK..LNRRLS	HPGHFWKSAE	L.....	.....
hKSR-2	TKLMDMLEKL	PK..RNRRLS	HPGHFWKSAE	L.....	.....
mKSR-2	TKLMDMLEKL	PK..RNRRLS	HPGHFWKSAE	L.....	.....
DmKSR	ARLLSLEHL	PKKRLARSPS	HPVNLSRSAE	SVF.....	.....
CeKSR	TDINLKL TAL	PKKPRVNRSP	SFPVMMKSYE	STF.....	.....

1001	
hKSR-1 (full)	SNPKM
mKSR-1	GNPKM
hKSR-1 (partial)	.....
hKSR-2	.....
mKSR-2	.....
DmKSR	.....
CeKSR	.....